

Db	6.1. RANGINTIA RUMEKI SEBANKU KUETT ANHWAHANU HAST KETRATK JEEBEKKU 120
Oy	121 LINNAMOGI CHITTEDE GEMORNGU LILHU TULLUOKKASPARA INI STANGU 180
Db	121 LINNAMOGI CHITTEDE GEMORNGU LILHU TULLUOKKASPARA INI STANGU 180
Oy	181 HUDEUDUNOKROKOKAYOKKA TUFTER SEBOSGUTTA MULBOSGUTTA 240
Db	181 HUDEUDUNOKROKOKAYOKKA TUFTER SEBOSGUTTA MULBOSGUTTA 240
Oy	241 TIGHASTESTAPU MALYKSPALMATTU LAVUJADSKYKOKKOKKAPPA 300
Db	241 TIGHASTESTAPU MALYKSPALMATTU LAVUJADSKYKOKKOKKAPPA 300
Oy	301 RODSEVARA MASAARJAKKAPPEKKA 311
Db	301 RODSEVARA MASAARJAKKAPPEKKA 311

The present sequence is human drug metabolizing enzyme (hcy-t) protein. Human hcy-t is nucleic acid molecule consisting of the amino acid, treatment and prevention of disorders associated with increase of decreased expression of DM. Examples of such disorders include, autoimmune/inflammatory disorder such as acquired immune deficiency syndrome (AIDS); rheumatoid arthritis; atopopathy; cell proliferative disorder such as melanoma; attherosclerosis; developmental disorders such as schizophrenia; metabolic disorder such as diabetes mellitus; eye disorder such as conjunctivitis; glaucoma; iritis; metabolic disorders such as Addison's disease; obesity; gastrointestinal disorder such as anorexia; dysphagia and hepatic tumours including cirrhotic hypertension; adenomas and carcinomas. DM hcy-t is useful for use to modulate human disease including DM, HCV or trichinella infestation (mice therapy). DM hcy-t is immunogenic fragment useful for screening libraries of compounds in several drug screening assays.

19-JUL-2001, 12-JAN-2001, 2001-MO-US01174.
 XX PP PR
 XX PR
 14-JAN-2001, 200005-0176119.
 XX PR
 28-JAN-2001, 200005-0176454.
 XX PA
 (INCY-) INCYTE GENOMICS INC.

```

RESULT 3
AB66121
AB66121 standard; protein; 331 AM
XX
AC
AB66121;
XX
DT 02-APR-2001 (first entry)
XX
DE Protein of the invention #33.

```


be used for tracking disorders of colon, brain, skin, heart, blood vessels, kidney, prostate, eye, muscle, ovary, testis and epididymis, bone marrow, lymphatic, and hematopoietic systems. T cells, fibroblasts, stem cells, precursor T cell neoplasms, bone forming cells, and bone marrow cells.

Query Match 99.8%; Score 1691; DB 22; Length 331;

Mayers B.;
WPI, 2002-11933/23.
WPI-PBD; A005714.
Human alcohol dehydrogenases (AHD) polyacetylenes and polypeptides, useful as tools for diagnosis or treating AHD-related or AHD-associated disorders, e.g. malignant breast metastases, seama or leukopenia

GARIBOLDI 173

sequence 331 aa)

AN076222 standard; protein; 331 AA; ID: XX

matches 330; conservative 0; Mismatches 1; Indels 0; Gaps 0

DT
XX
08-MAY-2002 (First entry)

1 MSRYLLPSALGTVGAAVLLDKYTGACPSKATIPGKTVITGANTGIGKOTALEAR 60

XX KW Alcohol dehydrogenase; ADH; human; cytosolic; a

THE JOURNAL OF CLIMATE

idiopathic inflammatory bowel disease, *ibd*

121 LINNAGVRCPHTIEDGZPBMQFGVNLGHPLTNNLJDKASAPSRINLSSLRVAG 180

KW lung disease; adult respiratory distress syndrome; skin disease; bronchitis; sarcoidosis; pneumothorax; colon disorder; colitis;

181 RIDDDLNWQTRKNTKAACQSKLAVLIFTKELSRALO3GVTNMLHPGVAXTELGRH 240

241 TAVISTOCK PICTURE BOOKS FOR CHILDREN 300

XX
PN

THE JOURNAL OF CLIMATE VOL. 19, 2006

24-JAN-2002.

30. EDETEVARLNEESARLUGLEAPSVEREQPLPR 331

PR 15-DBC-1999; 201

XX

Copyright (c) 1993 - 2004 Camprogen Ltd.

GenCore version 5.1.6
(c) 1993 - 2004 Camprogen Ltd.

OM protein - protein search, using SW model

Run on: February 9, 2004, 11:37:22 | Search time: 57 Seconds

Without alignments | Number of alignments: 1498.516 Million cell updates/sec

Title: US10-007-194a-16

Target score: 1693

Sequence: 1 NSKYLPIBLAQTGAGANL.....ESARLVLUGLAVLNSVPEQDPLPR 331

Scoring table: BLOSUM62

Gapcost: 10.0 | Gapext: 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830325

Maximum DB seq length: 0 | Maximum DB length: 200000000

Post-processing: Minimum Match 100% | Maximum Match 100%

Listing first 45 summaries

Database : SPARSEDB_11

1: SP_acetobacter*

2: SP_bacteri*

3: SP_fungi*

4: SP_invertebrates*

5: SP_mammal*

6: SP_micr*

7: SP_prokari*

8: SP_viruses*

9: SP_bacteria*

10: SP_plant*

11: SP_cocci*

12: SP_viruses*

13: SP_invertebrates*

14: SP_mammal*

15: SP_viruses*

16: SP_bacteri*

17: SP_archaea*

PRED: No. is the number of results predicted by chance to have a PRED score greater than or equal to the score of the result being printed, and is displayed by analysis of the total score distribution.

SUMMARIES

RESULT

No. | Score | Match | Length | DB ID | Description

No.	Score	Match	Length	DB ID	Description	
					PRELIMINARY	PNT
1	16188	98.6	331	4	QCB777 human manganese	331 AA.
2	14345	98.2	334	11	QCB777 human manganese	
3	1340	79.1	260	4	QBG688 human manganese	
4	1234	72.8	299	11	QBG688 human manganese	
5	818	49.3	310	5	QBG607 diatomophila	
6	812	47.9	310	5	QBG607 diatomophila	
7	802	47.3	310	5	QBG609 diatomophila	
8	802.5	47.3	310	5	QBG609 diatomophila	
9	79.5	46.6	266	5	QBG601 diatomophila	
10	76.7	45.3	300	5	QBG612 diatomophila	
11	74.5	44.0	316	11	QBG612 diatomophila	
12	73.9	43.6	318	4	QBG621 human sapiens	
13	73.9	43.6	318	4	QBG621 human sapiens	
14	73.9	43.6	318	4	QBG621 human sapiens	
15	73.8	43.6	318	11	QBG621 human sapiens	
16	73.8	43.6	318	4	QBG620 human sapiens	

ALIGNMENTS

RESULT

No. | Score | Match | Length | DB ID | Description

No.	Score	Match	Length	DB ID	Description	
					PRELIMINARY	PNT
1	17	73.7	5	43.5	316	4 QCB777 human sapiens
2	18	73.0	5	43.3	316	10 QCB777 human sapiens
3	19	73.0	5	43.3	293	11 QCB777 human sapiens
4	20	72.8	5	43.0	293	11 QCB777 human sapiens
5	21	72.6	5	42.8	316	4 QCB777 human sapiens
6	22	72.5	5	42.6	314	11 QCB776 human sapiens
7	23	71.5	5	42.2	315	11 QCB776 human sapiens
8	24	71.5	5	42.2	316	5 QCB776 human sapiens
9	25	68.6	5	40.3	11	QCB776 human sapiens
10	26	68.6	5	40.3	11	QCB776 human sapiens
11	27	68.6	5	40.3	16	QCB776 human sapiens
12	28	56.1	5	33.1	290	16 QCB776 human sapiens
13	29	56.1	5	32.3	211	16 QCB776 human sapiens
14	30	56.1	5	32.3	212	16 QCB776 human sapiens
15	31	55.4	5	31.5	318	16 QCB776 human sapiens
16	32	55.4	5	31.5	318	16 QCB776 human sapiens
17	33	53.0	5	31.4	314	16 QCB776 human sapiens
18	34	53.0	5	31.3	314	4 QCB776 human sapiens
19	35	53.0	5	31.3	314	4 QCB776 human sapiens
20	36	52.5	5	31.0	287	5 QCB776 human sapiens
21	37	52.3	5	30.9	110	16 QCB776 human sapiens
22	38	51.5	5	30.4	318	16 QCB776 human sapiens
23	39	51.5	5	30.4	318	16 QCB776 human sapiens
24	40	51.0	5	30.3	310	16 QCB776 human sapiens
25	41	51.0	5	30.3	406	16 QCB776 human sapiens
26	42	51.1	5	30.1	311	10 QCB772 human sapiens
27	43	50.5	5	29.8	210	11 QCB772 human sapiens
28	44	50.2	5	29.6	311	10 QCB772 human sapiens
29	45	49.7	5	29.4	314	4 QCB772 human sapiens
30	46	49.7	5	29.4	314	4 QCB772 human sapiens
31	47	49.7	5	29.4	314	4 QCB772 human sapiens
32	48	49.7	5	29.4	314	4 QCB772 human sapiens
33	49	49.7	5	29.4	314	4 QCB772 human sapiens
34	50	49.7	5	29.4	314	4 QCB772 human sapiens
35	51	49.7	5	29.4	314	4 QCB772 human sapiens
36	52	49.7	5	29.4	314	4 QCB772 human sapiens
37	53	49.7	5	29.4	314	4 QCB772 human sapiens
38	54	49.7	5	29.4	314	4 QCB772 human sapiens
39	55	49.7	5	29.4	314	4 QCB772 human sapiens
40	56	49.7	5	29.4	314	4 QCB772 human sapiens
41	57	49.7	5	29.4	314	4 QCB772 human sapiens
42	58	49.7	5	29.4	314	4 QCB772 human sapiens
43	59	49.7	5	29.4	314	4 QCB772 human sapiens
44	60	49.7	5	29.4	314	4 QCB772 human sapiens
45	61	49.7	5	29.4	314	4 QCB772 human sapiens
46	62	49.7	5	29.4	314	4 QCB772 human sapiens
47	63	49.7	5	29.4	314	4 QCB772 human sapiens
48	64	49.7	5	29.4	314	4 QCB772 human sapiens
49	65	49.7	5	29.4	314	4 QCB772 human sapiens
50	66	49.7	5	29.4	314	4 QCB772 human sapiens
51	67	49.7	5	29.4	314	4 QCB772 human sapiens
52	68	49.7	5	29.4	314	4 QCB772 human sapiens
53	69	49.7	5	29.4	314	4 QCB772 human sapiens
54	70	49.7	5	29.4	314	4 QCB772 human sapiens
55	71	49.7	5	29.4	314	4 QCB772 human sapiens
56	72	49.7	5	29.4	314	4 QCB772 human sapiens
57	73	49.7	5	29.4	314	4 QCB772 human sapiens
58	74	49.7	5	29.4	314	4 QCB772 human sapiens
59	75	49.7	5	29.4	314	4 QCB772 human sapiens
60	76	49.7	5	29.4	314	4 QCB772 human sapiens
61	77	49.7	5	29.4	314	4 QCB772 human sapiens
62	78	49.7	5	29.4	314	4 QCB772 human sapiens
63	79	49.7	5	29.4	314	4 QCB772 human sapiens
64	80	49.7	5	29.4	314	4 QCB772 human sapiens
65	81	49.7	5	29.4	314	4 QCB772 human sapiens
66	82	49.7	5	29.4	314	4 QCB772 human sapiens
67	83	49.7	5	29.4	314	4 QCB772 human sapiens
68	84	49.7	5	29.4	314	4 QCB772 human sapiens
69	85	49.7	5	29.4	314	4 QCB772 human sapiens
70	86	49.7	5	29.4	314	4 QCB772 human sapiens
71	87	49.7	5	29.4	314	4 QCB772 human sapiens
72	88	49.7	5	29.4	314	4 QCB772 human sapiens
73	89	49.7	5	29.4	314	4 QCB772 human sapiens
74	90	49.7	5	29.4	314	4 QCB772 human sapiens
75	91	49.7	5	29.4	314	4 QCB772 human sapiens
76	92	49.7	5	29.4	314	4 QCB772 human sapiens
77	93	49.7	5	29.4	314	4 QCB772 human sapiens
78	94	49.7	5	29.4	314	4 QCB772 human sapiens
79	95	49.7	5	29.4	314	4 QCB772 human sapiens
80	96	49.7	5	29.4	314	4 QCB772 human sapiens
81	97	49.7	5	29.4	314	4 QCB772 human sapiens
82	98	49.7	5	29.4	314	4 QCB772 human sapiens
83	99	49.7	5	29.4	314	4 QCB772 human sapiens
84	100	49.7	5	29.4	314	4 QCB772 human sapiens
85	101	49.7	5	29.4	314	4 QCB772 human sapiens
86	102	49.7	5	29.4	314	4 QCB772 human sapiens
87	103	49.7	5	29.4	314	4 QCB772 human sapiens
88	104	49.7	5	29.4	314	4 QCB772 human sapiens
89	105	49.7	5	29.4	314	4 QCB772 human sapiens
90	106	49.7	5	29.4	314	4 QCB772 human sapiens
91	107	49.7	5	29.4	314	4 QCB772 human sapiens
92	108	49.7	5	29.4	314	4 QCB772 human sapiens
93	109	49.7	5	29.4	314	4 QCB772 human sapiens
94	110	49.7	5	29.4	314	4 QCB772 human sapiens
95	111	49.7	5	29.4	314	4 QCB772 human sapiens
96	112	49.7	5	29.4	314	4 QCB772 human sapiens
97	113	49.7	5	29.4	314	4 QCB772 human sapiens
98	114	49.7	5	29.4	314	4 QCB772 human sapiens
99	115	49.7	5	29.4	314	4 QCB772 human sapiens
100	116	49.7	5	29.4	314	4 QCB772 human sapiens
101	117	49.7	5	29.4	314	4 QCB772 human sapiens
102	118	49.7	5	29.4	314	4 QCB772 human sapiens
103	119	49.7	5	29.4	314	4 QCB772 human sapiens
104	120	49.7	5	29.4	314	4 QCB772 human sapiens
105	121	49.7	5	29.4	314	4 QCB772 human sapiens
106	122	49.7	5	29.4	314	4 QCB772 human sapiens
107	123	49.7	5	29.4	314	4 QCB772 human sapiens
108	124	49.7	5	29.4	314	4 QCB772 human sapiens
109	125	49.7	5	29.4	314	4 QCB772 human sapiens
110	126	49.7	5	29.4	314	4 QCB772 human sapiens
111	127	49.7	5	29.4	314	4 QCB772 human sapiens
112	128	49.7	5	29.4	314	4 QCB772 human sapiens
113	129	49.7	5	29.4	314	4 QCB772 human sapiens
114	130	49.7	5	29.4	314	4 QCB772 human sapiens
115	131	49.7	5	29.4	314	4 QCB772 human sapiens
116	132	49.7	5	29.4	314	4 QCB772 human sapiens
117	133	49.7	5	29.4	314	4 QCB772 human sapiens
118	134	49.7	5	29.4	314	4 QCB772 human sapiens
119	135	49.7	5	29.4	314	4 QCB772 human sapiens
120	136	49.7	5	29.4	314	4 QCB772 human sapiens
121	137	49.7	5	29.4	314	4 QCB772 human sapiens
122	138	49.7	5	29.4	314	4 QCB772 human sapiens
123	139	49.7	5	29.4	314	4 QCB772 human sapiens
124	140	49.7	5	29.4	314	4 QCB772 human sapiens
125	141	49.7	5	29.4	314	4 QCB772 human sapiens
126	142	49.7	5	29.4	314	4 QCB772 human sapiens
127	143	49.7	5	29.4	314	4 QCB772 human sapiens
128	144	49.7	5	29.4	314	4 QCB772 human sapiens
129	145	49.7	5	29.4	314	4 QCB772 human sapiens
130	146	49.7	5	29.4	314	4 QCB772 human sapiens
131	147	49.7	5	29.4	314	4 QCB772 human sapiens
132	148					

Neoptera: Buprestidae; Diptera: Brachycera; Mecoptera?
 Odonata: Odonata; Orthoptera: Pyrgomorphidae; Grylloblattidae;
 Strepsiptera: Strepsiptera; Coleoptera: Curculionidae; Curculionidae;
 Dermaptera: Dermaptera; Diptera: Drosophilidae.
 [1] - TaxID:7227; OK

RC STRAIN=“miceKey”; RX MEDLINE=20160506; PubMed=10731132; RA HOLDNAGA, R.; EVANS, C. A.; GECASSE, J. D.; ADAMS, M. D.; CLARK, S. E.; HILL, R. A.; HODKIN, K. A.; GILLE, R. S.; ANNADASARI, P. G.; SCHERER, S. S.; LIPSON, M.; HODKIN, K. A.; GILLE, R. S.; DR SMITH, J. B.; BROWN, S. J.; BROWN, S. J.; PUBLISHER: PLoS ONE; PMID:31305; COR2664.

RA.	Spiller, B.	Spreading, A.C.	Sugden, M.	Strong, K.	Suh, B.	...
RA.	Svartek, R.	Tector, C.	Turner, R.	Vanter, E.	Wang, A.	Wang, X.
RA.	Wang, Z.-J.	Wasserman, D.A.	Weisbrock, G.M.	Weisbrock, J.	Werner, S.	...
RA.	Williams, S.M.	Woolridge, T.	Worley, K.C.	Wu, D.	Xiang, Y.	Yachayev, I.
Db						
Dy						
...						

Ra, Zheng X.-L., Zhong F.-N., Zhong K.-X., and S.-J. and X.-J. Shuakai, R.-C., Gibson R.-A., Myers B.-W., Rubin G.-M., Venter J.-C., and P.-T. The genome sequence of *Drosophila melanogaster*. *PNAS* 92: 2873-2888 (2005).

- CATALYTIC ACTIVITY: Chlorophyllide A + NAD(+) = protoclorophyllide + NADPH + CO₂ (CO₂ release).
- PATRICK H. COOPERSON, C. COOPERSON
- SEMI-ELIMINATIVE BELONGS TO THE SHORT-CHAIN DEHYDROGENASES / REDUCTASES (EDR) FAMILY. POR SUSP.FAMILY.

CC This software is copyright. It is produced through a
CC collaboration between the Swiss Institute of Bioinformatics and the
CC European Bioinformatics Institute. There are no restrictions on its
CC use. By non-profit institutions as long as the
CC modified and a reference are made. See [http://www.ebi.ac.uk/annotation/](http://www.ebi.ac.uk/annotation/CC)
CC modified and a reference are made. See <http://www.ebi.ac.uk/annotation/>
CC modified and a reference are made. See <http://www.ebi.ac.uk/annotation/>

REINHARDT, R. J. 1996. Cloning and characterization of the nuclear gene for NADH protochlorophyllide oxidoreductase. *Plant Mol. Biol.* 31:57-71 (1996). <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=PubMed&term=9519259>

- CATALYTIC ACTIVITY: Chlorophyllide A + NAD(+) = protoclorophyllide + NADPH + CO₂ (CO₂ release).
- PATRICK H. COOPERSON, C. COOPERSON
- SEMI-ELIMINATIVE BELONGS TO THE SHORT-CHAIN DEHYDROGENASES / REDUCTASES (EDR) FAMILY. POR SUSP.FAMILY.

CC This software is copyright. It is produced through a
CC collaboration between the Swiss Institute of Bioinformatics and the
CC European Bioinformatics Institute. There are no restrictions on its
CC use. By non-profit institutions as long as the
CC modified and a reference are made. See [http://www.ebi.ac.uk/annotation/](http://www.ebi.ac.uk/annotation/CC)
CC modified and a reference are made. See <http://www.ebi.ac.uk/annotation/>
CC modified and a reference are made. See <http://www.ebi.ac.uk/annotation/>

UK: *Light energy* → *ATP* → *Reduction* → *Chlorophyll biosynthesis*; Oxidoreductase: NADP, KW: Photosynthesis; Chlorophyll biosynthesis; Chlorella; Transit Peptide.

```

RESULT 3
OKR, STRAT STANDARD; PRT; 298 A.
ID 01121-1994 (Rel. 29, Created)
ID 01-110-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1986 (Rel. 14, Last annotation update)

```

AL-SITE 298 AA; 31415 MW; DDD244156632E10C CRC64;
SEQUENCE

Quest Match	20.91;	Score 33.5;	DB: 1;	Length 298;		
Best Local Similarity	11.91;	Score 3.4;	DB: 1;	Length 298;		
Matches	99;	Conservative	42;	Mismatches	128;	Gap 6;
Quest Match	20.91;	Score 33.5;	DB: 1;	Length 298;		
Best Local Similarity	11.91;	Score 3.4;	DB: 1;	Length 298;		
Matches	99;	Conservative	42;	Mismatches	128;	Gap 6;
36	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95				
Y	3	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
Db	96	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
	63	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
	63	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
	155	MLLDDKIKASPRINNSLARVHADIDPQKRTKTKTAKOSLQSLVLTFLC	214			
Y	119	MLLDDKIKASPRINNSLARVHADIDPQKRTKTKTAKOSLQSLVLTFLC	214			
Db	120	MLLDDKIKASPRINNSLARVHADIDPQKRTKTKTAKOSLQSLVLTFLC	214			
	215	BRQGQ	269			
Y	179	BRQGQ	269			
Db	270	BRQGQ	269			
	237	TRVLLASPLGLDTQYRDFDQGTAHQLPDAFLW	288			
Quest Match	20.91;	Score 33.5;	DB: 1;	Length 297;		
Best Local Similarity	11.91;	Score 3.4;	DB: 1;	Length 297;		
Matches	99;	Conservative	42;	Mismatches	128;	Gap 6;
36	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95				
Y	3	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
Db	96	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
	63	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
	63	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
	155	MLLDDKIKASPRINNSLARVHADIDPQKRTKTKTAKOSLQSLVLTFLC	214			
Y	119	MLLDDKIKASPRINNSLARVHADIDPQKRTKTKTAKOSLQSLVLTFLC	214			
Db	215	BRQGQ	269			
Quest Match	20.91;	Score 32.1;	DB: 1;	Length 297;		
Best Local Similarity	11.91;	Score 3.4;	DB: 1;	Length 297;		
Matches	99;	Conservative	42;	Mismatches	128;	Gap 6;
36	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95				
Y	3	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
Db	96	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
	62	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
	62	IRKTVLVTGANTGKQLLARQGNTILQARMEKEAAQDQIGRTLNHYNH	95			
	155	MLLDDKIKASPRINNSLARVHADIDPQKRTKTKTAKOSLQSLVLTFLC	214			
Y	119	MLLDDKIKASPRINNSLARVHADIDPQKRTKTKTAKOSLQSLVLTFLC	214			
Db	215	BRQGQ	269			

(EDB) FAMILY FOR STUDENTS
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There is no restriction on its use, modified and this statement is not removed. Usage for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

ENGLJ X15869 ; CAA33879 ; 1 ; - .
HTRP ; 5047193 ; 504733 .
HTRP ; P14601 ; 1PD2 .
InterPro : IPR002198 ; ADR short .
InterPro : IPR005979 ; Procl short .

PF00116; adn; short; 1-
TIGR0187; TIGR0187; LP01; 1-
Photocatalysis; Chloroplycide biosynthesis; Oxidoreductase; NADP;
Chloroplast; Transl peptid; Multigene family.
TRANSIT 1 74
THAIN 75 388
PROTOCHLOROPHYLLID REDUCTASE A.

```

SEQUENCE 388 AA; 41151 MW: EB308F133096C129 CRC64;
  Match 20.2%; Score 342; DB 1/1; Length 3.88;
  Similarity 30.9%; Pred. No. 6.1e-18;
  Local Similarity 30.9%; Conserv. 46%; Mismatches 126/ 18;
  Matches 129/ 18; Indels 104/ 18;
  Gaps 18/ 18;
  % coverage: 100.00000000000000;
  % complete: 100.00000000000000;
  % query: 100.00000000000000;
  % target: 100.00000000000000;

```

7.5 ADIRETPIAHYRNBHDLASLXKIBEPKAKI BEBEVYDILINNAGYORCPHWT---T 135
 1.16 AK---AAGNDSTWMLDLASDQVCPQTFQFRAMPLDVYCHAA1YPTARTPFT 173
 13.6 EDGFFENPONVHGFPLTMLA1DCL_KASASII1-----NLS 173

1.74 ADGHENISGVNHNIGHFLANLMBOLGDYSRMTYVOSTIGNTNLAYNPPAALG 233
 1.74 SLAHVAG ----- HIFDODANTRKNTKAYCOKSLAUYTFLKLSRL-BOSGV 223
 1.74 DLRGLAGGSAGSAMIDCB ----- SPGAKAYDKSYCQNL-TMCDFRHYHGYI 287

224 FVNLHPPG-VARTELGRBTGHSPTSTLAPFHWY-KSPPLAOPSTYLA-VATE 279
 288 TYSLLPACHTGTLFRE--HIPS--KLIPPPQFQPTKQFVSAREGRLLQVVAEP 342
 290 LADVSKYFQDLCQAP---APADEHEVRLMAESELQCL 319

343 VLTTSVNMNSNNSA S FENCL SQUAED PESKRTWELSEN VOL 387

Q15781 (Ref. 40, Created)
16-OCT-2001 (Ref. 40, Last sequence update)
28-FEB-2003 (Ref. 41, Last annotation update)
Prochlorophyllide reductase A, chloropredoxin precursor (EC 1.3.1.31)
(NADPH:prochlorophyllide oxidoreductase A) (POR A).

PODA
Triticum aestivum (Wheat)
Vitellaria paradoxa
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae;
Tribe: Triticeae; Triticum.
NCBI_TaxID: 4565.

[1] SEQUENCE FROM N.A.

100

๘๗

Archaeoglobus archaeoglobus At5290 (Reported) Archaeobacterium tumefaciens (strain CS8, Duport) plasmid pAB1105